What is claimed is:

1. An isolated polynucleotide encoding a polypeptide comprising a PIN1 PPIase that does not contain a WW domain.

2. An isolated polynucleotide that:

(a) encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:2; and

(b) does not encode a WW domain.

3. An isolated polynucleotide comprising the polynucleotide sequence of SEQ ID NO:1, wherein said polynucleotide does not encode for a WW domain.

4. An isolated polypeptide comprising the amino acid sequence of SEQ ID NO:2, wherein said polypeptide does not contain a WW domain.

5. An isolated polynucleotide that

(a) encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:4; and

(b) does not encode a WW domain.

6. An isolated polynucleotide comprising the polynucleotide sequence of SEQ ID NO:3, wherein said polynucleotide does not encode a WW domain.

7. An isolated polypeptide comprising the amino acid sequence of SEQ ID NO:4, wherein said polypeptide does not contain a WW domain.

8. A polynucleotide according to claim 2, further comprising at least one polynucleotide sequence that encodes a proteolytic cleavage site.

9. A polynucleotide according to claim 5, further comprising at least one polynucleotide sequence that encodes a proteolytic cleavage site.

10. A polynucleotide according to claim 8, wherein the proteolytic cleavage site is a thrombin cleavage site.

11. A polynucleotide according to claim 9, wherein the proteolytic cleavage site is a thrombin cleavage site.

12. A polynucleotide according to claim 2, further comprising at least one polynucleotide sequence that encodes a histidine tag.

13. A polynucleotide according to claim 5, further comprising at least one polynucleotide sequence that encodes a histidine tag.

14. An isolated polypeptide encoded by the polynucleotide of claim 1.

15. An isolated polypeptide encoded by the polynucleotide of claim 6.

16. An isolated polypeptide encoded by the polynucleotide of claim 7.

17. A vector comprising the polynucleotide of claim 1.

18. A vector according to claim 17, wherein said vector is an expression vector comprising the polynucleotide of claim 1 operably linked to a promoter.

19. A eukaryotic cell line or prokaryotic cell transformed or transfected with the vector of claim 17.

20. A eukaryotic cell line or prokaryotic cell transformed or transfected with a polynucleotide comprising the polynucleotide of claim 1.

21. A method of producing a polypeptide or fragment thereof comprising culturing the cell line or cell of claim 19 under conditions such that said polypeptide is expressed, and recovering said polypeptide.

22. A method of assaying a compound for its PIN1 modulating ability comprising:

(a) adding a test compound to a polypeptide comprising a PIN1 peptidyl-prolyl isomerase, wherein said polypeptide does not contain a WW domain;

(b) measuring said polypeptide's peptidyl-prolyl isomerase activity; and

(c) determining if the activity of the polypeptide is modulated by said test compound.

23. A method according to claim 22, wherein said polypeptide is encoded by a polynucleotide comprising the polynucleotide of claim 2 or 5.

24. A method according to claim 22, wherein said method is done in a high-throughput format.

25. A crystal structure comprising a PIN1 peptidyl-prolyl isomerase (PPIase) polypeptide that does not contain a WW domain.

26. A crystal structure comprising the polypeptide encoded by the polynucleotide of claim 2, or a fragment thereof.

27. A crystal structure comprising the polypeptide encoded by the polynucleotide of claim 5, or a fragment thereof.

28. A crystal structure according to claim 25, wherein said crystal structure diffracts X-rays at a resolution value greater than or equal to 3 Å.

29. A crystal structure according to claim 25, wherein said crystal structure diffracts X-rays at a resolution value of greater than or equal to 2 Å.

30. A crystal structure comprising a PIN1 PPIase polypeptide:ligand complex, wherein said polypeptide does not contain a WW domain.

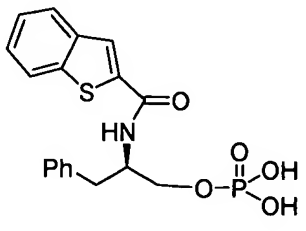
31. A crystal structure according to claim 30, wherein said polypeptide is encoded by the polynucleotide sequence of claim 2 or 5.

32. A crystal structure according to claim 30, wherein said crystal structure diffracts X-rays at a resolution of greater than or equal to 3.0 Å.

33. A crystal structure according to claim 25, wherein said PIN1 peptidyl-prolyl isomerase polypeptide has a three-dimensional structure characterized by the structure coordinates of Table II.

34. A crystal structure according to claim 30, wherein said ligand is a modulator of PIN1 peptidyl-prolyl isomerase activity.

35. A crystal structure according to claim 34, wherein said modulator of PIN1 peptidyl-prolyl isomerase activity is a compound of the formula:



36. A crystal structure according to claim 30, wherein said PIN1 PPIase polypeptide has a three-dimensional structure characterized by the structure coordinates of Table III.

37. A method of using a three-dimensional structure of a complex comprising a PIN1 peptidyl-prolyl isomerase polypeptide devoid of the WW domain and compound I, as defined by the structure coordinates of Table III or a portion thereof, in a drug discovery strategy comprising:

(a) selecting a potential drug using computer-aided drug design with the three-dimensional structure determined from one or more sets of atomic coordinates in Table III, wherein said selecting is performed in conjunction with computer modeling;

(b) contacting said potential drug with a polypeptide containing a functional PIN1 peptidyl-prolyl isomerase; and

(c) detecting the binding of said potential drug with said polypeptide.

38. A method of using a three-dimensional structure of a complex comprising a PIN1 peptidyl-prolyl isomerase polypeptide devoid of the WW domain and compound I and as defined by the structure coordinates of Table III, or a portion thereof, in a drug discovery strategy comprising:

(a) selecting a potential drug using computer-aided drug design with the three-dimensional structure determined from one or more sets of structure coordinates in Table III, wherein said selecting is performed in conjunction with computer modeling;

(b) contacting said potential drug with a polypeptide containing a functional PIN1 peptidyl-prolyl isomerase; and

(c) determining if said potential drug modulates the peptidyl-prolyl isomerase activity of a polypeptide containing a PIN1 peptidyl-prolyl isomerase.

39. A method for evaluating the potential of a chemical entity to associate with a molecule or molecular complex comprising a binding pocket defined by a set of structure coordinates comprising structure coordinates of PIN1 PPIase amino acids

His59, Leu61, Lys63, Ser67, Arg68, Arg69, Cys113, Leu122, Met130, Gln131, Phe134, Glu135, Thr152, Ser154, and His157, according to Table III, or a portion thereof, comprising the steps of:

(a) employing computational means to perform a fitting operation between the chemical entity and a binding pocket defined by structure coordinates of PIN1 PPIase amino acids His59, Leu61, Lys63, Ser67, Arg68, Arg69, Cys113, Leu122, Met130, Gln131, Phe134, Gli135, Thr152, Ser154, and His157, according to Table III; and

(b) analyzing the results of said fitting operation to quantify the association between the chemical entity and the binding pocket.

40. A method according to claim 39, wherein said set of structure coordinates comprises structure coordinates of PIN1 PPIase amino acids Arg54, Arg56, His59, Leu61, Lys63, Ser67, Arg68, Arg69, Ser72, Trp73, Ser111, Asp112, Cys113, Ser114, Ser115, Ala116, Lys117, Ala118, Arg119, Gly120, Asp121, Leu122, Gly123, Ala124, Phe125, Ser126, Arg127, Gly128, Gln129, Met130, Gln131, Lys132, Pro133, Phe134, Glu135, Thr152, Asp153, Ser154, and His157 according to Table III.

41. A method according to claim 39, wherein said method evaluates the potential of a chemical entity to associate with a molecule or molecular complex defined by structure coordinates of substantially all of the PIN1 PPIase amino acids, as set forth in Table III.

42. A method for identifying a modulator of a molecule comprising a PIN1 PPIase substrate-binding domain comprising the steps of:

(a) using a set of structure coordinates comprising structure coordinates of PIN1 PPIase amino acids His59, Leu61, Lys63, Ser67, Arg68, Arg69, Cys113, Leu122, Met130, Gln131, Phe134, Glu135, Thr152, Ser154, and His157, according to Table III to generate a three-dimensional structure of a molecule comprising a PIN1 PPIase or PPIase-like substrate-binding pocket;

(b) employing said three-dimensional structure to design or select said modulator;

(c) synthesizing or obtaining said modulator; and

(d) contacting said modulator with said molecule to determine the ability of said modulator to interact with said molecule.

43. A method according to claim 42, wherein said set of structure coordinates used in step (a) comprises PIN1 PPIase amino acids Arg54, Arg56, His59, Leu61, Lys63, Ser67, Arg68, Arg69, Ser72, Trp73, Ser111, Asp112, Cys113, Ser114, Ser115, Ala116, Lys117, Ala118, Arg119, Gly120, Asp121, Leu122, Gly123, Ala124, Phe125, Ser126, Arg127, Gly128, Gln129, Met130, Gln131, Lys132, Pro133, Phe134, Glu135, Thr152, Asp153, Ser154, and His157 according to Table III.

44. A method according to claim 43, wherein the structure coordinates used in step (a) comprise substantially all the amino acids of PIN1 PPIase according toTable III.

45. A machine-readable medium having stored thereon data comprising the structure coordinates of a PIN1 PPIase substrate-binding site amino acids His59, Leu61, Lys63, Ser67, Arg68, Arg69, Cys113, Leu122, Met130, Gln131, Phe134, Glu135, Thr152, Ser154, and His157 according to Table III.

46. A machine-readable medium having stored thereon data comprising the structure coordinates of a PIN1 PPIase substrate-binding site comprising amino acids Arg54, Arg56, His59, Leu61, Lys63, Ser67, Arg68, Arg69, Ser72, Trp73, Ser111, Asp112, Cys113, Ser114, Ser115, Ala116, Lys117, Ala118, Arg119, Gly120, Asp121, Leu122, Gly123, Ala124, Phe125, Ser126, Arg127, Gly128, Gln129, Met130, Gln131, Lys132, Pro133, Phe134, Glu135, Thr152, Asp153, Ser154, and His157 according to Table III.

47. A machine-readable medium having stored thereon data comprising the structure coordinates of a PIN1 PPIase:Compound I complex according to Table III.

48. A method of obtaining structural information about a molecule or a molecular complex of unknown structure by using the structure coordinates set forth in Table III, comprising the steps of:

(a) generating X-ray diffraction data from said crystallized molecule or molecular complex; and

(b) applying at least a portion of the structure coordinates set forth in Table III to said X-ray diffraction pattern to generate a three-dimensional electron density map of at least a portion of the molecule or molecular complex.

49. A method for evaluating the ability of a compound to associate with a molecule or molecular complex comprising a PIN1 PPIase substrate-binding pocket, said method comprising the steps of:

(a) constructing a computer model of said binding pocket defined by a set of structure coordinates comprising structure coordinates of PIN1 PPIase amino acids His59, Leu61, Lys63, Ser67, Arg68, Arg69, Cys113, Leu122, Met130, Gln131, Phe134, Glu135, Thr152, Ser154, and His157 according to Table III;

(b) selecting a compound to be evaluated by a method selected from the group consisting of (i) assembling molecular fragments into said compound, (ii) selecting a compound from a small molecule database, (iii) *de novo* ligand design of said compound, and (iv) modifying a known modulator, or a portion thereof, of a peptidyl-prolyl isomerase;

(c) employing computational means to perform a fitting program operation between computer models of said compound to be evaluated and said binding pocket in order to provide an energy-minimized configuration of said compound in the binding pocket; and

(d) evaluating the results of said fitting operation to quantify the association between said compound and the binding pocket model, thereby evaluating the ability of said compound to associate with said binding pocket.

50. A method according to claim 49, wherein said binding pocket is defined by a set of structure coordinates comprising structure coordinates of PIN1 PPIase:compound I complex amino acids Arg54, Arg56, His59, Leu61, Lys63, Ser67, Arg68, Arg69, Ser72, Trp73, Ser111, Asp112, Cys113, Ser114, Ser115, Ala116, Lys117, Ala118, Arg119, Gly120, Asp121, Leu122, Gly123, Ala124, Phe125, Ser126, Arg127, Gly128, Gln129, Met130, Gln131, Lys132, Pro133, Phe134, Glu135, Thr152, Asp153, Ser154, and His157 according to Table III.

51. A method for identifying a modulator of a molecule comprising a PIN1 PPIase substrate-binding site, comprising the steps of:

(a) constructing a computer model of said binding pocket defined by a set of structure coordinates comprising structure coordinates of PIN1 PPIase substrate-binding site amino acids His59, Leu61, Lys63, Ser67, Arg68, Arg69, Cys113, Leu122, Met130, Gln131, Phe134, Glu135, Thr152, Ser154, and His157 according to Table III;

(b) selecting a compound to be evaluated as a potential modulator by a method selected from the group consisting of (i) assembling molecular fragments into said compound, (ii) selecting a compound from a small molecule database, (iii) *de novo* ligand design of said compound, and (iv) modifying a known inhibitor, or a portion thereof, of a protein kinase;

(c) employing computational means to perform a fitting program operation between computer models of said compound to be evaluated and said binding pocket in order to provide an energy-minimized configuration of said compound in the binding pocket;

(d) evaluating the results of said fitting operation to quantify the association between said compound and the binding pocket model, thereby evaluating the ability of said compound to associate with said binding pocket;

(e) synthesizing said compound; and

(f) contacting said compound with said molecule to determine the ability of said compound to modulate the peptidyl-isomerase activity of said molecule.

52. The method according to claim 51, wherein a set of structure coordinates comprises structure coordinates of PIN1 PPIase substrate-binding amino acids Arg54, Arg56, His59, Leu61, Lys63, Ser67, Arg68, Arg69, Ser72, Trp73, Ser111, Asp112, Cys113, Ser114, Ser115, Ala116, Lys117, Ala118, Arg119, Gly120, Asp121, Leu122, Gly123, Ala124, Phe125, Ser126, Arg127, Gly128, Gln129, Met130, Gln131, Lys132, Pro133, Phe134, Glu135, Thr152, Asp153, Ser154, and His157 according to Table III are used to generate said three-dimensional structure of the molecule comprising a PIN1 PPIase-like binding pocket.

53. A method for screening compounds for PIN1 PPIase modulating activity comprising the steps of:

(a) providing an assay buffer containing a Pintide-PIN1 PPIase polypeptide complex;

(b) adding a test compound; and

(c) measuring the disruption of the Pintide-PIN1 PPIase complex.

54. A method according to claim 53, wherein said method is done in a high-throughput format.

55. A method according to claim 53, wherein said Pintide is labeled with fluorescein.

56. A method according to claim 55, wherein said disruption of the Pintide-PIN1 complex is measured using fluorescence-polarization.